09/639453
AMT #9
2/22/02

=> s stable integration
L1 1294 STABLE INTEGRATION

=> s integrat?
L2 662657 INTEGRAT?

=> s stable
L3 1148711 STABLE

=> s l2(3n)l3
L4 2506 L2(3N) L3

=> s splice or splices or spliced or splicing
L5 116070 SPLICE OR SPLICES OR SPLICED OR SPLICING

=> s l4 and l5
L6 20 L4 AND L5

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7 7 DUP REM L6 (13 DUPLICATES REMOVED)

=> s l2 and l5
L8 1871 L2 AND L5

=> dup rem l8
PROCESSING IS APPROXIMATELY 61% COMPLETE FOR L8
PROCESSING COMPLETED FOR L8
L9 815 DUP REM L8 (1056 DUPLICATES REMOVED)

=> s l3 and l2 and l5
L10 108 L3 AND L2 AND L5

=> dup rem l10
PROCESSING COMPLETED FOR L10
L11 43 DUP REM L10 (65 DUPLICATES REMOVED)

=> s l11 and py<1997
1 FILES SEARCHED...
3 FILES SEARCHED...
4 FILES SEARCHED...
L12 23 L11 AND PY<1997

=> d l12 ibib abs 1-23

L12 ANSWER 1 OF 23 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1996:461696 BIOSIS
DOCUMENT NUMBER: PREV199699184052
TITLE: Reverse ***splicing*** of the Tetrahymena IVS: Evidence for multiple reaction sites in the 23S rRNA.
AUTHOR(S): Roman, Judibelle; Woodson, Sarah A. (1)
CORPORATE SOURCE: (1) Dep. Chem. Biochem., Univ. Maryland, College Park, MD 20742-2121 USA
SOURCE: RNA (New York), (1995) Vol. 1, No. 5, pp. 478-490. ISSN: 1355-8382.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Group I introns in rRNA genes are clustered in highly conserved regions that include tRNA and mRNA binding sites. This pattern is consistent with insertion of group I introns by direct interaction with exposed regions of rRNA. ***Integration*** of the Tetrahymena group I intron (or intervening sequence, IVS) into large subunit rRNA via reverse ***splicing*** was investigated using E. coli 23S rRNA as a model substrate. The results show that sequences homologous to the ***splice*** junction in Tetrahymena are the preferred site of ***integration*** , but that many other sequences in the 23S rRNA provide secondary targets. Like the original ***splice*** junction, many new reaction sites are in regions of ***stable*** secondary structure. Reaction at the natural ***splice*** junction is observed in 50S subunits and to a lesser extent in 70S ribosomes. These results support the feasibility of intron transposition to new sites in rRNA genes via reverse ***splicing*** .

L12 ANSWER 2 OF 23 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1996:438397 BIOSIS
DOCUMENT NUMBER: PREV199699152003
TITLE: Expression of the Volvox gene encoding nitrate reductase: Mutation-dependent activation of cryptic ***splice*** sites and intron-enhanced gene expression from cDNA.
AUTHOR(S): Gruber, Heribert; Kirzinger, Stefan H.; Schmit, Rudiger (1)
CORPORATE SOURCE: (1) Lehrstuhl GeneTIK, Univ. Regensburg, Universitaetsstrasse 31, D-93040 Regensburg Germany
SOURCE: Plant Molecular Biology, (1996) Vol. 31, No. 1, pp. 1-12. ISSN: 0167-4412.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Use of the nitrate reductase encoding gene (nitA) as selection marker has facilitated the successful nuclear transformation of Volvox carteri. The Volvox nitA gene contains 10 introns. A ***stable*** nitA mutation in the Volvox recipient strain 153-81 resides in a G-to-A transition of the first nucleotide in the 5' ***splice*** site of nitA intron 2. This mutation resulted in at least three non-functional ***splice*** variants, namely: (1) intron 2 was not ***spliced*** at all; (2) a cryptic 5' ***splice*** site 60 nt upstream or (3) a cryptic 5' ***splice*** site 16 nt downstream of the mutation were activated and used for ***splicing*** . When we used nitA cDNA (pVcNR13) for transformation of V. carteri 153-81, a low efficiency of about 5 times 10-5 transformants per reproductive cell was observed. Re-***integration*** of either intron 1 (pVcNR15) or introns 9 and 10 (pVcNR16) in the transforming cDNA increased transformation rates to 5 times 10-4. In parallel, pVcNR15-transformed Volvox exhibited growth rates that were 100-fold increased over the pVcNR13transformed alga. This intron-enhancement of nitA gene expression appears to be associated with post-transcriptional processing and 'channelling' of the message. These data suggest an important role of ***splicing*** for gene expression in V. carteri.

L12 ANSWER 3 OF 23 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1996:332262 BIOSIS
DOCUMENT NUMBER: PREV199699054618
TITLE: Insertional tagging cloning, and expression of the Toxoplasma gondii hypoxanthine-xanthine-guanine phosphoribosyltransferase gene. Use as a selectable marker for ***stable*** transformation.
AUTHOR(S): Donald, Robert G. K.; Carter, Darrick; Ullman, Buddy; Roos, David S. (1)
CORPORATE SOURCE: (1) Dep. Biol., Univ. Pennsylvania, Philadelphia, PA 19104-6018 USA
SOURCE: Journal of Biological Chemistry, (1996) Vol. 271, No. 24, pp. 14010-14019. ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
AB A nonhomologous ***integration*** vector was used to identify the Toxoplasma gondii hypoxanthine-xanthine-guanine phosphoribosyl transferase (HXGPRT) gene by insertional mutagenesis. Parasite mutants resistant to 6-thioxanthine arose at a frequency of apprx 3 times 10-7. Genomic DNA flanking the insertion sites was retrieved by marker rescue and used to identify molecular clones exhibiting unambiguous homology to H(X)GPRT genes from other species. Sequence analysis of vector/genome junction sites reveals that ***integration*** of the linearized vector occurred with minimal rearrangement of either vector or target sequences, although the addition of filler DNA and small duplications or deletions of genomic sequences at the transgene termini was observed. Two differentially ***spliced*** classes of cDNA clones were identified, both of which complement hpt and gpt mutations in Escherichia coli. Kinetic analysis of purified recombinant enzyme revealed no significant differences between the two isoforms. Internally deleted clones spanning the genomic locus were used to create "knock-out" parasites, which lack all detectable HXGPRT activity. Complete activity could be restored to these knock-out mutants by transient transformation with either genomic DNA or cDNA-derived minigenes encoding both enzyme isoforms. ***Stable*** HXGPRT+ transformants were isolated under selection with mycophenolic acid, demonstrating the feasibility of HXGPRT as both a positive and